

Please replace the paragraph beginning at page 5, line 4, with the following rewritten paragraph:

Figure 1 depicts a nucleotide sequence of mouse *Fkh<sup>sf</sup>* cDNA (SEQ ID NO: 1); translation is predicted to initiate at position 259 and terminate at position 1546.

Please replace the paragraph beginning at page 5, line 7, with the following rewritten paragraph:

Figure 2 depicts the amino acid sequence of mouse *Fkh<sup>sf</sup>* (SEQ ID NO: 2).

Please replace the paragraph beginning at page 5, line 9, with the following rewritten paragraph:

Figure 3 depicts a nucleotide sequence of 1735 bp corresponding to human *FKH<sup>sf</sup>* cDNA (SEQ ID NO: 3; including a 1293 bp coding region); translation is predicted to initiate at position 55 and terminate at position 1348.

Please replace the paragraph beginning at page 5, line 12, with the following rewritten paragraph:

Figure 4 depicts the sequence of a 431 amino acid human *FKH<sup>sf</sup>* protein (SEQ ID NO: 4).

Please replace the paragraph beginning at page 34, line 4, with the following rewritten paragraph:

A complementary DNA (cDNA) encoding the complete mouse *Fkh<sup>sf</sup>* protein may be obtained by a reverse-transcriptase polymerase chain reaction (RT-PCR) procedure. More specifically, first-strand cDNA is generated by oligo dT priming 5 ug of total RNA from a suitable source (eg., mouse spleen) and extending with reverse transcriptase under standard conditions (eg., Gibco/BRL SuperScript kit). An aliquot of the first-strand cDNA is then subjected to 35 cycles of PCR (94°C for 30 sec, 63°C for 30 sec, 72°C for 2 min) in the presence of the forward and reverse

primers (Forward primer: GCAGATCTCC TGA<sup>CT</sup>CTGCC TTC; SEQ ID NO: 5; Reverse primer: GCAGATCTGA CAAGCTGTGT CTG; SEQ ID NO: 6) (0.2 mM final concentration), 60 mM Tris-HCl, 15 mM ammonium sulfate, 1.5 mM magnesium chloride, 0.2 mM each dNTP and 1 unit of Taq polymerase.

Please replace the paragraph beginning at page 34, line 18, with the following rewritten paragraph:

A human *FKH<sup>sf</sup>* cDNA encoding the complete *FKH<sup>sf</sup>* protein may be obtained by essentially the same procedure as described in Example 2. In particular, starting with total spleen RNA, and utilizing the following oligonucleotide primers (Forward primer: AGCCTGCCCT TGGACAAGGA C; SEQ ID NO: 7); Reverse primer: GCAAGACAGT GGAAACCTCA C; SEQ ID NO: 8), and the same PCR conditions outlined above, except with a 60°C annealing temperature.

Please replace the paragraph beginning at page 35, line 11, with the following rewritten paragraph:

As an example, a 360 bp DNA fragment is amplified from 1<sup>st</sup> strand cDNA using the following oligos:

DMO5985 (forward): CTACCCACTGCTGGCAAATG (ntd. 825-844 of Figure. 1)  
(SEQ ID NO: 9)

DMO6724 (reverse): GAAGGAACTATTGCCATGGCTTC (ntd 1221-1199)  
(SEQ ID NO: 10)

Please replace the paragraph beginning at page 35, line 20, with the following rewritten paragraph:

The PCR products are run on an 1.8% agarose gel, transferred to nylon membrane and probed with end-labeled oligonucleotides that are complementary to the region corresponding to the site of the Scurfy-specific 2 bp insertion. Two separate hybridization reactions are performed to detect the normal and Scurfy PCR products, using the oligonucleotides below (the site of the 2 bp insertion is shown in bold):

Normal: ATGCAGCAAGAGCTCTTGTCCATTGAGG (SEQ ID NO: 11)  
DMO7439

Scurfy: GCAGCAAGAGCTCTTTTGTCCATTGAGG (SEQ ID NO: 12)  
DMO6919

Please replace the paragraph beginning at page 40, line 19, with the following rewritten paragraph:

The unique features of the *FKH<sup>sf</sup>* gene sequence may be used to identify other novel genes (and proteins) which fall into the same sub-class of forkhead-containing molecules. The *FKH<sup>sf</sup>* protein is unique in its having a single zinc finger domain amino-terminal to the forkhead domain as well as in the extreme carboxy-terminal position of the forkhead domain. A degenerate PCR approach may be taken to isolate novel genes containing a zinc finger sequence upstream of a forkhead domain. By way of example, the following degenerate primers were synthesized (positions of degeneracy are indicated by parentheses, and "I" indicates the nucleoside inosine):

Forward primer: CA(TC)GGIGA(GA)TG(CT)AA(GA)TGG (SEQ ID NO:13)

Reverse primer: (GA)AACCA(GA)TT(AG)TA(AGT)AT(CT)TC(GA)TT (SEQ ID NO:14)

#### REMARKS

The enclosed electronic and paper copies of the Sequence Listing include no new matter that goes beyond the original application as filed, but are supplied as requested by the